

Education

- 2017–2021 **Bachelor of Engineering, Bioinformatics & Systems biology**, School of Life Science & Technology, Huazhong University of Science & Technology, Wuhan.
- Comprehensive exposure to the core areas of Bioinformatics;
 - Two years project on microbiome (especially the human gut microbiome)
- 2018–2020 **Bioinformatics and Deep learning**, Coursera, Online.
- Completed courses:
- *Finding Hidden Messages in DNA* by **Pavel A. Pevzner** and **Phillip Compeau**;
 - *Bioinformatics: Introduction and Methods* by **Ge Gao** and **Liping Wei**;
 - *Deep Learning Specialization I, II, and III* by **Andrew Ng**.

Publications

Articles

- 2021 Yuguo Zha[§], **Hui Chong**[§], Pengshuo Yang[§], and Kang Ning. Microbial dark matter: from discovery to applications (revised, *Genomics, Proteomics & Bioinformatics*). 2021.
- 2021 Yuguo Zha, **Hui Chong**, and Kang Ning. Microbiome sample comparison and search: From pair-wise calculations to model-based matching. *Frontiers in Microbiology*, volume 12, page 781. Frontiers, 2021.
- 2021 **Hui Chong**, Qingyang Yu, Yuguo Zha, Guangzhou Xiong, Nan Wang, Xinhe Huang, Shijuan Huang, Chuqing Sun, Sicheng Wu, Wei-Hua Chen, et al. Expert: Transfer learning-enabled context-aware microbial source tracking (submitted, *Science Advances*). *bioRxiv*. Cold Spring Harbor Laboratory, 2021.
- 2021 Tao Bai, Xue Zhu, Xiang Zhou, Denise Grathwohl, Pengshuo Yang, Yuguo Zha, Yu Jin, **Hui Chong**, Qingyang Yu, Nora Isberner, et al. Reliable and interpretable mortality prediction with strong foresight in covid-19 patients: An international study from china and germany. *Frontiers in artificial intelligence*, page 112. Frontiers, 2021.
- 2020 Yuguo Zha[§], **Hui Chong**[§], Hao Qiu, Kai Kang, Yuzheng Dun, Zhixue Chen, Xuefeng Cui, and Kang Ning. Ontology-aware deep learning enables ultrafast, accurate and interpretable source tracking among sub-million microbial community samples from hundreds of niches (under revision, *Genome Medicine*). *bioRxiv*. Cold Spring Harbor Laboratory, 2020.
- 2020 Kai Kang[§], **Hui Chong**[§], and Kang Ning. Meta-prism 2.0: Enabling algorithm for ultra-fast, accurate and memory-efficient search among millions of microbial community samples (under revision, *GigaScience*). *bioRxiv*. Cold Spring Harbor Laboratory, 2020.
- 2020 Maozhen Han, Yuguo Zha, **Hui Chong**, Chaofang Zhong, and Kang Ning. Utilizing microbiome approaches to assist source tracking, treatment and prevention of covid-19: Review and assessment. *Computational and structural biotechnology journal*. Elsevier, 2020.

Research Experience

Fudan University, Research Assistant

Jul, 2021 – *Global microbial gene synteny survey.*

present Generation of syntenic graphs based on the entire GMGC dataset. Extraction and hypothesis testing of syntenic patterns. Implementation of the analysis pipeline.

Advisor: **Dr. Luis Pedro Coelho** ([Lab](#) [Web-page](#))

Jul, 2021 – *Global antimicrobial peptides survey.*

present Designed a website for global antimicrobial peptides. Constructed the website based on Python, FastAPI, Vue.js, Quasar, Plotly.js, and SQLite3.

Advisor: **Dr. Luis Pedro Coelho**

Huazhong University of Science and Technology, Research Assistant (Undergraduate)

Apr, 2021 – *Cross-region generalization of disease model based on Transfer Learning and selected biomarkers.*

Jul, 2021 Project administration. Conceptualization of the idea and the approach. Study design. Project member training. Technical support on data processing, modeling, cross-validation, and visualization. Manuscript writing & editing.

Advisor: **Prof. Kang Ning** ([Lab](#) [Web-page](#)) and **Prof. Weihua Chen** ([Lab](#) [Web-page](#))

Aug, 2020 – *Application of transfer learning approach for analyzing the spatial/temporal dynamics of human gut microbiome.*

present Project administration. Conceptualization of the project. Project member training.

Advisor: **Prof. Kang Ning**

Aug, 2020 – *Developing a transfer learning approach for high-throughput microbial source tracking.*

present Project administration. Conceptualization of the idea and the approach. Implementation of the approach using TensorFlow + sqlite + Pandas. Application of microbial source tracking in disease pattern analysis and temporal pattern analysis. Implementation of feature extractor module using TensorFlow. Python package distribution of the approach. Manuscript writing, editing & submission.

Advisor: **Prof. Kang Ning** and **Prof. Weihua Chen**

Oct, 2019 – *Developing an ontology-aware approach for fast and accurate microbial source tracking.*

Aug, 2020 Feature engineering module design and implementation utilizing Treelib + NumPy + Scikit-learn. Feature selection of 125,823 community samples. Parallelization of SourceTracker using Foreach + doParallel. Performance comparison with SourceTracker and JSD. Case-studies for ONN4MST, FEAST, JSD, and SourceTracker. Manuscript editing, data analysis & visualization.

Advisor: **Prof. Kang Ning**

May, 2019 – *Developing a cell sorter using Convolutional Neural Network and Transfer learning (Training program).*

Nov, 2019 Developing a cell sorter program using CNN architecture and Transfer learning. Design and implementation of the data processing pipeline and the CNN model. Cross-validation of the CNN model and another ResNet-based CNN model.

Advisor: **Prof. Yu Xue** ([Lab](#) [Web-page](#))

Position of Responsibility

Nov, 2021 – **Steering committee member of Microbiome Virtual International Forum**, Event present backstage administrator and website administrator.

Projects

EXPERT	Context-aware microbial source tracking based on transfer learning. <i>Link</i>
ONN4MST	Hierarchical microbial source tracking based on deep learning. <i>Link</i>
AMPSphere website	Website for retrieving and analyzing Antimicrobial Peptide candidates around the globe. <i>Link</i>
Meta-Prism	Ultra-fast, accurate and memory-efficient microbial community search accelerated by Single Instruction Multiple Data. <i>Link</i>
UniPCoA	Unifrac-based PCoA visualization of microbial community samples. <i>Link</i>
living tree	Taxonomical abundance remapping and feature engineering for metagenomic samples. <i>Link</i>
Functional CrossRef	Resources for cross-database conversion of functional terms: KO number, GO (Gene Ontology) term, EC (Enzyme Commission) number, and MetaCyc reaction/pathways ID. <i>Link</i>

Research skills

Scientific computing	Python, Pandas, NumPy, SciPy, TensorFlow, R, Linux shell
Programming skills	Top-down programming, Object-oriented programming, Parallelized programming
Reproducible research	Git, GitHub, Jupyter lab
Statistics & visualization	Pandas, ggplot, plotnine, Plotly, Adobe Illustrator

Referees

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